

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 9, 2003, 12:23:23 ; Search time 15 Seconds
(without alignments)
83.316 Million cell updates/sec

Title: US-09-632-429-4
Perfect score: 89
Sequence: 1 WEVLQWTWETCER 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	57.3	292	2 S70117	hypothetical prote
2	49	55.1	395	2 B96610	hypothetical prote
3	46	51.7	427	2 T41257	hypothetical prote
4	46	51.7	1080	2 T19048	probable Pro-X car
5	46	51.7	1121	2 T21303	hypothetical prote
6	46	51.7	1230	2 S47466	cellulose 1,4-beta
7	44	49.4	203	2 A53294	superoxide dismuta
8	43	48.3	536	2 T10000	cytochrome P450 (C
9	43	48.3	524	2 T09999	cytochrome P450 -
10	43	48.3	524	2 T09944	probable cytochrom
11	42	47.2	347	2 D69373	immunogenic protei
12	42	47.2	475	2 T45766	hypothetical prote
13	42	47.2	501	2 B85025	hypothetical prote
14	42	47.2	569	2 S75169	urease (EC 3.5.1.5
15	42	47.2	731	2 T09172	probable calcium-a
16	41.5	46.6	359	2 A22421	3-dehydroshikimate
17	41.5	46.6	519	2 S36808	methylmalonyl-CoA
18	41	46.1	242	2 E71621	ERCC1-like excisio
19	41	46.1	276	2 T47351	hypothetical prote
20	41	46.1	278	2 S48776	hypothetical prote
21	41	46.1	306	2 A75316	hypothetical prote
22	41	46.1	330	2 S08500	QUTG protein - Eme
23	41	46.1	340	2 B31277	hypothetical prote
24	41	46.1	481	2 T10036	hypothetical prote
25	41	46.1	494	2 T16658	hypothetical prote
26	41	46.1	575	2 A96766	unknown protein F2
27	41	46.1	594	2 D71347	conserved hypothet
28	41	46.1	732	2 Ad0014	primosomal protein
29	41	46.1	856	2 G96814	hypothetical prote

30	41	46.1	951	2 T00260	hypothetical prote
31	41	46.1	1085	2 H82511	hypothetical prote
32	41	46.1	1711	2 T21432	hypothetical prote
33	40.5	45.5	1256	2 T47325	hypothetical prote
34	40.5	45.5	4861	2 S71752	giant protein p619
35	40	44.9	280	2 A70513	hypothetical prote
36	40	44.9	295	2 S46749	hypothetical prote
37	40	44.9	306	2 D87531	glycosyl transfera
38	40	44.9	415	2 T49840	hypothetical prote
39	40	44.9	416	2 G86232	cysteine proteinas
40	40	44.9	614	2 T19963	hypothetical prote
41	40	44.9	741	2 B49555	enhancer of split
42	40	44.9	855	2 T29775	hypothetical prote
43	39.5	44.4	348	2 JN0250	dehydroshikimate d
44	39.5	44.4	551	2 D75195	hypothetical prote
45	39	43.8	93	2 AC3330	hypothetical prote

ALIGNMENTS

RESULT 1

S70117

hypothetical protein YDR287w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein p9819.7

C:Species: Saccharomyces cerevisiae

C>Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002

C:Accession: S70117

R:Fulton, L.

submitted to the EMBL Data Library, May 1996

A:Description: The sequence of S. cerevisiae cosmid 9819.

A:Reference number: S70114

A:Accession: S70117

A:Molecule type: DNA

A:Residues: 1-292 <FUI>

A:Cross-references: EMBL:U51031; NID:gl332635; PID:gl332637; GSPDB:GN00004; MIPS:YDR2

C:Genetics:

A:Gene: MIPS:YDR287w

A:Cross-references: SGD:S0002695

A:Map position: 4R

C:Superfamily: suppressor protein subB

Query Match 57.3%; Score 51; DB 2; Length 292;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WEVLQWTWETC 11

DB 223 WEGGCWAWDVC 233

RESULT 2

B96610

hypothetical protein T8L23.7 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: B96610

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Huiziar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96610

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-395 <STO>

A:Cross-references: GB:AE005173; NID:gl11055860; PIDN:AAG28328.1; GSPDB:GN00141

Query. Match 51.7%; Score 46; DB 2; Length 1080;

A:Accession: D69373
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-347 <KLE>
A:Cross-references: GB:AE001036; GB:AE000782; NID:g2680359; PIDN:AAB90255.1; PID:g264961
C:Superfamily: immunogenic protein BCSP31

Query Match 47.2%; Score 42; DB 2; Length 347;
Best Local Similarity 54.5%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCE 12
|||:|:|
Db 35 EVKPSWATCD 45

RESULT 12
T45766
hypothetical protein F24M12.390 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 20-Jun-2000
C:Accession: T45766
R:Vitale, D.; Liguori, R.; Flores, M.; Argiriou, A.; De Simone, V.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23012
A:Accession: T45766
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-475 <VIT>
A:Cross-references: EMBL:AL132980
A:Experimental source: cultivar Columbia; BAC clone F24M12
C:Genetics:

A:Map position: 3
A:Introns: 100/2; 147/3; 225/2; 302/2; 319/2; 356/3; 375/3; 399/1
A:Note: F24M12.390
C:Superfamily: Arabidopsis thaliana hypothetical protein F24M12.380

Query Match 47.2%; Score 42; DB 2; Length 475;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLWCWTWETCE 12
|:|:|:|
Db 15 VVCGWGERCE 24

RESULT 13
E85025
hypothetical protein AT4g01990 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: E85025
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: E85025
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <STO>
A:Cross-references: GB:NC_001268; NID:g7268583; PIDN:CAB80692.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g01990
A:Map position: 4

Query Match 47.2%; Score 42; DB 2; Length 501;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEVLCWTWE 9
|||:|:|:|
Db 341 WESTCWTYD 349

RESULT 14
S75169
urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
N:Alternate names: protein sll1750
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75169
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75169
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-569 <KAN>
A:Cross-references: EMBL:D90903; GB:AB001339; NID:gl652127; PIDN:BAAL7083.1; PID:g165
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:

A:Gene: ureC
C:Superfamily: urease 62K chain; urease 62K chain homology
C:Keywords: hydrolase; metalloprotein; nickel
F:5-552/Domain: urease 62K chain homology <U62>
F:136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted

Query Match 47.2%; Score 42; DB 2; Length 569;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVLCWTWETCER 13
||:|:|:|
Db 371 EVICRTWQTAHK 382

RESULT 15
T09172
probable calcium-activated potassium channel KCNN3 - human
C:Species: Homo sapiens (man)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T09172
R:Chandy, K.G.; Fantino, E.; Wittekindt, O.; Kalman, K.; Tong, L.L.; Ho, T.H.; Gutman Mol. Psychiatry 3, 32-37, 1998
A:Title: Isolation of a novel potassium channel gene hSKCa3 containing a polymorphic

A:Reference number: Z16601; MUID:98150774; PMID:9491810
A:Accession: T09172
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-731 <CHA>
A:Cross-references: EMBL:AF031815; NID:g3309530; PID:g3309531
C:Genetics:
A:Gene: KCNN3
C:Keywords: potassium channel; schizophrenia

Query Match 47.2%; Score 42; DB 2; Length 731;
Best Local Similarity 46.2%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 WEVLCWTWETCER 13
|:|:|:|
Db 471 WIIAAWTVRACER 483

Search completed: January 9, 2003, 12:25:09
Job time : 16 secs